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Result
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Listing first 45 summaries
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Human HM1.24 antig
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Amino acid sequenc	Bacterial general	Smooth muscle myos		Rattus norvegicus	Nucleolar/endosoma	sophila mel	H. pylori GHPO 363	#29 human	AMML chromosome in		Human protein SEQ		Amino acid sequenc			prot		Low density lipopr	LOX-1	-	nsity lipo	S	Polypeptide #2 for	ORFX OF	Human HM1.24 antig	.24 antige	24 antigenic		ble	4 antigeni	in encode	n boun	Human colon cancer

## ALIGNMENTS

RESULT AAR72703

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AAR72703 standard; Protein; 180

AΑ

Rheumatoid arthritis; diagnosis; pre-B cell growth; enhancement.

for enhancing pre-B cell growth.

Human membrane 06-DEC-1995 AAR72703;

(first entry) polypeptide

Claim 1; Page 29-30; 40pp; Japanese Recombinant membrane protein enhancing monoclonal antibody recognising it and rheumatoid arthritis N-PSDB; AAQ89606. WPI; 1995-161738/21. Hirano T, Kaisho T; 15-OCT-1993; 14-OCT-1994; 20-APR-1995 WO9510536-A Homo sapiens (HIRA/) HIRANO 93JP-0281622 94WO-JP01732 pre-B cell growth - and useful in the diagnosis of

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RESULT
AAW65771
ID AAW6
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Best Local
               The protein having the amino acid sequence below is bound specifically by a cytotoxic antibody which can be used in the treatment of lymphocytic tumours, including T-cell tumours and B-cell tumours other than myeloma. The antibody is preferably monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or humanised, and preferably contains a human antibody constant region C gamma (such as C gamma 1 or C gamma 3). A preferred antibody is qamma thi-human HM1.24 antibody or an antibody which binds to an epitope recognising anti-human HM1.24 antibody. The cytotoxic antibody is useful in the treatment of lymphocytic tumours such as acute or chronic B lymphocytic leukaemia,
       pre-B
                                                                                                                                                                          Claim
                                                                                                                                                                                                  Treatment of lymphocytic tumours using cytotoxic antibody - bin to specific antigen such as HM1.24 and effective against T-cell tumours and B-cell tumours other than myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A membrane polypeptide has been isolated from rheumatoid arthritis patients. The polypeptide supports pre-B-cell growth and is useful as an antigen for generating monoclonal antibodies for diagnosing rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                  Koishihara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein recognised by anti-human HM1.24 antibody.
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DB; AAV07579.
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     lymphoma,
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       Burkitt's
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Burkitt's lymph
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smatches 0;
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     or
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Best Local Similarity
             complimentarity determining regions (CDR) of mouse origin, leading to a reshaped humanised antibody. The C regions are human Ck (L-chain) an human C gamma (especially C gamma 1) (H-chain). The FR regions of the L chain V region are derived from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. FR1-3 from human antibody HG3 and FR4 from human antibody HG3 regions of the H chain V region are derived from human antibody HG3 (e.g. FR1-3 from human antibody HG3 and FR4 from human antibody HG3 (e.g. FR1-3 from human antibody HG3 and FR4 from human antibody HG3 (e.g. FR1-3 from human antibody HG3 and FR4 from human antibody HG3 (e.g. FR1-3 from human antibody HG3 and FR4 from hum
                                                                                                                                                                                                                    A humanised anti-HM1.24 antibody has been developed which comprises human L and H Chain C regions, and L and/or H Chain V regions containing material originating in mouse anti-HM1.24 antibody. The V regions contain framework (FR) regions of human origin and
                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                Humanised anti-HM1.24 antibody -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koishihara Y,
Yoshimura Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 man; humanised; anti-HM1.24 antibody; myeloma; FR; CDR;
region; complimentarity determining region; antigenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-HM1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kosaka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96JP-0264756
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                                                                                                                                                                                                                                                                                                                              210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohtomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ŧ,
The antibodies are used at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             889; DB 19;
. No. 6.2e-78;
smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ono
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuchiya
                                                                                                                                                                                                                                                                                                                                                                           of myeloma
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Matches 180;
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                                                                                                                                                                                                            WPI;
                   which can be used to study the expression of HM1.24 antigen, promoter activity of its promoter region, and in development of drugs in treating e.g. myeloma and rheumatoid arthritis. This sequence represents the human HM1.24 antigenic protein described in the invention.
                                                               This invention describes a novel human antigenic protein, HM1.24, its encoding nucleic acid, splice variants and promoter region. The products of the invention have antirheumatic and antiarthritic activity. The DNA of the invention is isolated from bone marrow tumour cells,
                                                                                                                          Example
                                                                                                                                                  rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                        Antigenic protein;
antiarthritic; bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (especially 5-100) mg/kg body weight. The humanised antibody has low antigenicity and is therefore effective therapeutically in humans.
Sequence
                                                                                                                                                                                                                                 Ohtomo T,
                                                                                                                                                                                                                                                        (CHUS ) CHUGAI
                                                                                                                                                                                                                                                                               25-FEB-1998;
24-MAR-1998;
                                                                                                                                                                                                                                                                                                                  25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                        02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                               WO9943803-A1
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human HM1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY33202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY33202 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttlnhklqdasaeverlrrenqvlsvriadkkyypssqdsssaaapqllivllglsallq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
                                                                                                                                                  DNA encoding HM1.
s, useful e.g. in
oid arthritis -
                                                                                                                         1; Fig 1-2;
                                                                                                                                                                                                AAZ09726
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                                                                                                                                                                                                                                                                                                                                                                                                            ritic; bone rheumatoid
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180
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A
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98JP-0093883.
                                                                                                                                                                                                                                                                                                                 99WO-JP00884
                                                                                                                                                                                                                                                                                                                                                                                                                    HM1.24; splice variant; promoter; antirheumatic;
e marrow; tumour cell; drug development; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                 ĭ
                                                                                                                        83pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                            marrow; tumour ce
arthritis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                         X
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                 Koishihara
                                                                                                                                                           .24 antigen production in development
                                                                                                                                                          antigen protein as velopment of drugs :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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Pred. No. 6.2e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
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                                                                                                                                                                                                                                 Y,
                                                                                                                                                                                                                                 Kosaka
                                                                                                                                                             for
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                                                                                                                                                                       well as splicing
                                                                                                                                                           treating myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV

Query Match Best Local S Matches 180

al Similarity 180; Conser

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Score 889; DB 20; Pred. No. 6.2e-78; Mismatches 0;

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                                                                                                                                                                                               This sequence represents a human soluble HM1.24 antigenic protein. The invention relates to an immunochemical assay of anti-HM1.24 antibody by use of a soluble HM1.24 antigenic protein, or an immunochemical assay of the soluble antigen by use of the antibody. The immunoassay of the HM1.24 antigen or antibody is useful for diagnosis of immune disorders and cancer, for monitoring of anti-HM1.24 antigody immunotherapy, and for assay of the antibody or antigen for investigative purposes, in biological samples such as blood, serum, urine, milk, synovial fluid or microorganism culture media. The method is sensitive down to 500 pg/ml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-518836/43
N-PSDB; AAZ10917.
                                                                                                                            Sequence
                                                                                                                                                                               antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 14-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoassay useful for o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koishihara Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis
                                                                                                                            180 AA;
100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of anti-HM1.24 antibody or soluble HM1.24 antigen diagnosis of immune disorders and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ozaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigenic
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Pred. No. 6.2e-78;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                                                                                                                                                                   of the HM1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                        Query Match
Best Local
                                                                                                                                            Matches
                                                                                                                                                                                                                      The specification describes a reconstituted human antibody recognizing the peptide antigen HM1.24. This human antibody contains natural human framework regions modified by amino acid substitutions to provide homogeneity with a previously designed framework region (which may arise from a human or non-human source); and complementary determining regions (CDR) derived from a non-human anti-HM1.24 antibody. The reconstituted antibody is useful in the treatment of diseases in which the surface antigen HM1.24 is implicated such as myeloma. The present sequence represents HMI.24 antigenic protein.
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reconstituted human antibody; peptide antigen HM1.24; framework region; complementary determining region; CDR; anti-HM1.24 antibody; myeloma;
                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 131-133; 256pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                Reconstituted human antibody useful in the
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-277273/23
                                                                                                                                                                                                                                                                                                                                                                                                                          Tsuchiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09918212-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       humanised antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY02576
                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMI.24 antigenic protein
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                                                                                                                                                        Local Similarity
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                                                                                            MECRNYTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MECRNYTHLLQQELTEAQKGFQDVEAQAATCNHTYMALMASLDAEKAQGQKKVEELEGEI
                                                mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
                                                                                                                                            180;
                                                                                                                                                                                                                                                                                                                                                                                        AAX59485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                    180
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                    AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-0271726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-JP04469
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Pred.
                                                                                                                                            Mismatches
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                                                                                                                                        e 889; Db ...
1. No. 6.2e-78;
                                                                                                                                                                                                                                                                                                                                                                 treatment
                                                                                                                                            Indels
                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                 of myeloma
                                                                                                                                          0;
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AAY07250
ID AAY0
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                                                                                                                                                                                                  Matches 180;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody potentiator; lymphoid tumour; lymphoma; cytotoxic antibody; multiple myeloma; acute B-lymphocytoma; chronic B-lymphocytoma; pre-B lymphoma; Burkitt's lymphoma; acute T-lymphocytoma; therapy; chronic T-lymphocytoma; PNTL.
                                                                                                                                                                                                                                                                                       a cytotoxic antibody is potentiated by administration of a biological response modifier. The method can be used for treatment of lymphomas and multiple myelomas which are resistant to conventional treatment, such as acute B-lymphocytoma, chronic B-lymphocytoma, pre-B lymphoma, Burkitt's
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
             AAY07250
                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1998;
14-OCT-1997;
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                      This sequence represents a potentiator for an antibody against
                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                  Potentiation of antibody treatment of lymphoma with biological response modifier
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koishihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHUS ) CHUGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09918997-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potentiator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY05484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY05484 standard; Protein;
                                                                  121
                                                                                       121
                                                                                                                                                                                                                                                                                                                                             ymphoid
                                                                                                            61
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                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                   invention relates to a method for the treatment of lymphoma,
                                                                                                                                                      TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ
                                                                                                                                  MECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-277447/23
                                                                                                           mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX36561
            standard;
                                                                                                                                                                                                                                                                                                                                             tumour.
                                                                                                                                                                                                                                                                                                                                                                             Page
                                                                                                                                                                                                                                                                             acute T-lymphocytoma, chronic T-lymphocytoma, and PNTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲
                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            37-38; 62pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98JP-0222024
97JP-0280759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody
            Protein;
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                                                                                                                                                                                                                                                                                                                                                                           Japanese.
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                                                                                                                                                                                                  0,
                                                                                                                                                                                                 Score 889; DB 20;
Pred. No. 6.2e-78;
; Mismatches 0;
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                                                                                                                                                                                                                       180;
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                            Human; HM1.24 antigen protein; detection; pl multiple myeloma; plasmocytic leukaemia; ext multiple plasmocytoma; asymptomatic myeloma.
                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the mouse BST-2 protein which is used to raise antibodies, especially the monoclonal antibody RS38. The antibody can i used in compositions to treat myelomas when the antibody is associated with a cytotoxic activity.
                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ān
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 10; 13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY07250;
        30-MAR-2000
                          WO200017395-A1
                                                                                                 Human HM1.24 antigen
                                                                                                                    21-JUL-2000
                                                                                                                                      AAY53273;
                                                                                                                                                         AAY53273 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytotoxic
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                                                                                                                                                                                                                                                                           1999-283503/24.
DB; AAX29996.
                                                                                                                                                                                                                                                 MECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEI 120
                                           sapiens
                                                                                                                                                                                                                                        mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
                                                                                                                                                                                                                                                                                                                   180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BST-2; monoclonal antibody; RS38; myeloma;
                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                   (first entry)
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                                                                                                protein sequence
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                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                 Score 889; DB 20;
Pred. No. 6.2e-78;
Mismatches 0;
                                                                                                                                                        A
                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          an antibody
                                                                      extramedullary
                                                                                                 Ħ
                                                                              plasmocytoma;
                                                                                                 NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                  Indels
                                                                      plasmocytoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a sample at an early stage of disease development. The method comprises amplifying a polynucleotide which is expressed specifically or strongly in plasmocytomas before quantifying the amplification product by comparing with results obtained with a control sample. The method is for detecting or measuring plasmocytomas, applicable for early diagnosis of e.g. multiple myeloma, plasmocytic leukaemia, isolated plasmocytoma extramedullary plasmocytoma, multiple plasmocytoma brained from smoking or asymptomatic myeloma. The present sequence represents human HM1.24 antipen protein, which is expressed in plasmocytomas and so can be used the method of the control of t
                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection or measurement of plasmocytomas, applicable for early diagnosis of e.g. multiple myeloma and plasmocytic leukemia, us polynucleotide which is expressed specifically or strongly in
                                                                                        undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;
                                                                                                                                                                                                                                                       Ovarian tumour marker gene; human; overexpression; uprequepithelial tumour; cancer; diagnosis; prognosis; disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                     serous cystadenocarcinoma; mucinous cystadenocarcinoma;
mucinous cystadenoma; borderline mucinous tumour; endom
                                                                                                                                                                                                                            epithelial tumour; cancer; diagnosis; prognosis; disease monidentification; serous cystadenoma; borderline serous tumour;
                                                                                                                                                                                                                                                                                                                              Bone marrow stromal antigen (BST-2) ovarian tumour marker protein,
                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                           ABB50295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB50295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawai S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koishibara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 15-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 6.2e-78;
Mismatches 0;
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                                                                                                                                                                                     endometrioid carcinoma
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isease monitoring;
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RESULT 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83181-ABA83122, ABA83180, ABA83181 and ABA83184) or segments thereof (ABA83123-ABA83129, ABA83179, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenoma, borderline serous tumour.
  AAB70697 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenocarcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenocalcinoma, undifferentiad carcinoma, clear cell adenocarcinoma, cystadenocibroma, adenocibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent
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                                                                                                                                                                                                                                                                                                                                                                 Conservative
  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ovarian tumour marker genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                   .0%; Score 889; DB 22; .0%; Pred. No. 6.2e-78;
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RESULT 1
AAG73947
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Best Local Similarity 100.0%;
Matches 180; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; HM1.24 antigen expression potentiator; HM1.24 protein antigen; myeloma; interferon alpha; interferon gamma; IFN-alpha; IFN-gamma; interferon regulatory factor 2; IRF-2; cytostatic; cytotoxic antibody
AAG73947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \rm HM1.24 antigen expression potentiating agent containing interferon alpha or gamma or IRF-2 for treatment of myeloma -
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N-PSDB; AAF74792.
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16-FEB-2000; 2000JP-0038689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen.
standard;
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Pred. No. 6.2e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                            inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                   present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer-associated nucleic acid molecules (N)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding useful for preventing,
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                    Pages 666 to 682 and page 7053 of the ing at time of publication, meaning no ID NO:1027 to 1052, 7921 and 7922.
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ttlnhklqdasaeverlrrenqvlsvriadkkyypssqdsssaaapqllivllglsallq
                                                           mecrnvthllqqelteaqkgfqdveaqaatcnhtvmalmasldaekaqgqkkveelegei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer antigen
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arcinoma; chromosome 19.
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99US-0163280.
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Pred. No. 6.8e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lymphocyte activation inhibitor comprises antibodies, particular anti-HM1.24 antibody - for preventing and treating auto:immune diseases, rejection reactions in organ transplant or allergy
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Protein encoded by clone 0238_1.
                                                            12-MAY-1998
                                                                                                                   AAW36951;
                                                                                                                                                                       AAW36951 standard;
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                                                                                                                                                                       Protein; 197
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Human; secreted protein; molecular weight marker; genetic fingerprinting; antibody production; nutritional supplement; therapy; clone 0238\_1;

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                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a protein encoded by clone 0238_1, which is a colonymucleotide of the invention. The DNA encoding this sequence was isolated from a human dendritic cell cDNA library. The polynucleotide, which encodes a secreted protein, can be used, e.g. as a tissue or molecular weight marker, in genetic fingerprinting, to raise anti-protein or anti-DNA antibodies and in interaction trap assays. The protein can be used to assay biological activity, raise antibodies for use in immunoassays, as a marker, to identify inhibitors of its interactions and as a nutritional supplement. It may also have a very wide range of therapeutic and biological activities (no examples are given to support this), e.g. cytokine or modulator of cell proliferation and differentiation, immunostimulant or immunosuppressant, haematopoiesis regulator, bone, cartilage, tendon, ligament and/or nerve tissue growth stimulator, chemotactic/chemokinetic, thrombolytic or anti-inflammatory agent, antimicrobial, blorhythm, metabolism or behaviour modifier, anti-depressant or analgesic corrections.
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Best Local :
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Spaulding V;
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                                                                                                                                    AAY32763;
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Pred. No. 1.7e-73; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-518836/43.
N-PSDB; AAZ10915.
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoassay of anti-HM1.24 antibody or soluble HM1.24 useful for diagnosis of immune disorders and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koishihara Y,
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                                                                   MASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQ 158
dsssaaapqllivllglsallq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ozaki Y;
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95.1%;
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Q9YMP5;
01-MAY-1999 (TrEMBLrel. 10, COLOMAY-1999 (TrEMBLrel. 10, ICOLOMEC-2001 (TrEMBLrel. 19, ICDORF-82 PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1999) to the EMBL/GenBank/DDBJ database EMBL; AF081810; AAC770268.1; -.
InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
SEQUENCE 778 AA; 87841 MW; 811B8ED172CE9E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
Slavicek J.M., Rohrmann G.F.;
"Sequence and analysis of the genome of a baculovirus pathogenic for
Lymantria dispar.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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105 EKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSS 161
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                                                                       LKAQSELNRD-LQAKAEAQADANARLQAEIDSLKR----AESDAADLRNRVAQLEAEAES
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y.,
Fuji F., Hirama C., Nakamura Y., O
                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
FLAGELLAR PROTEIN REQUIRED FOR FLAGELLAR FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison wit Nucleic Acids Res. 28:4317-4331(2000).
EMBL: APO01519; BAB07319.1; -.
MEROPS; M37.UPW; -.
                       Flagella;
                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=86665;
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Fuji F., Hirama C., Nakamura Y., Ogasawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
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01-DEC-2001
                                             EMBL;
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Pfam; PF01551; Peptidase_M37; 1.
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                                                                                                                 Horikoshi K.;
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                                                                                             "Complete genome sequence of the alkaliphilic bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=20014706; PubMed=10545595;

MEDLINE=2014706; Domizawa M., Ota M.,

Oka A., Tamiya G., Tomizawa M., Ota M.,

Shiina T., Yoshitome M., Lizuka M., Sass

Kawakubo Y., Sugai J., Ozawa A., Ohkido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                  LQLELSRAQEARRWW---
                                                                                                                                                                               LSVRIA----DKKYYPSSQDSSSAAAPQLLIVLLGLSA 177
                                                                                                                                                                                                               LMVQLKAQELEHSDSVKQLKGQVASLQEKVTSQSQEQAILQRSLQDKAAEVEVERMGAKG
                                                                                                                                                                                                                                               LMASLDAEKAQGQKKVEELEGEITTLNHK-----
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31; Conserv
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(TrEMBLrel.
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24.7%;
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Pred. No. 0.13
34; Mismatches
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Pred. No. 1.4;
34; Mismatches
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Last annotation update)
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Last annotation updat
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Catarrhini;
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Sasao Y., Iwashita
kido M., Kimura M.,
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a K.,
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                                                                           Shiina S., Tamiya G., Oka A., I "Homo sapiens 2,229,817bp genom Submitted (SEP-199) to the EMB EMBL; AB029343; BA882158.1; -EMBL; AP000509; BAB63313.1; -SEQUENCE 756 AA; 85951 MW;
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01-NOV-1999
01-DEC-2001
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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"A candidate gene for psoriasis near HLA-C, HCR (pg8), is highly polymorphic with a disease-associated susceptibility allele.";
Hum. Mol. Genet. 9:1533-1542(2000).
EMBL; AFZ16493; ABF74221.1;
-
SEQUENCE 756 AA; 86058 MW; 8E4D03358B62DEB4 CRC64;
                                                                                                                                                                                                                 Oka A., Tamiya G., Makino S., Tomizawa M., Yar Watanabe K., Yamazaki M., Tashiro H., Kimura I "HCR-a-helix colled-coll rod homologue.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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Hirakawa M., Yamag
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  RDGLRAVME - -
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                      40; Conserv
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(SEP-1999) to
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(TremBLrel. 12, Last sequence up
(TremBLrel. 19, Last annotation
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 -CRNVTHLL---QQELTEAQKGFQDVEAQ-AATC---
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genomic DNA of 6p21
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e EMBL/GenBank/DDBJ
                       32;
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Pred. No. 1.4;
34; Mismatches
                      Score 104.5;
Pred. No. 1.4;
32; Mismatches
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Best Local
TISSUE=COLON MUCOSA;
Watanabe K., Kumagai A., Itak
Suzuki Y., Obayashi M., Nishi
Nakamura Y., Isogai T., Sugan
"NEDO human cDNA sequencing p
Submitted (FEB-2000) to the E
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SEQUENCE 782 AA; 88616 MW; F472FE544F627CE
                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
CDNA FLJ20210 FIS, CLONE COLF1787.
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSVRI-----ADKKYYPSSQDSSSAAAPQLLIVLLGLSA 177
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(TrEMBLrel. 15, Last a
(TrEMBLrel. 15, Cast a
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25.2%;
                                             Nishi T., S
Sugano S.;
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  project.";
EMBL/GenBank/DDBJ
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Pred. No. 1.7;
32; Mismatches
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                                                                                                                                                                                                           Craniata; Vo
Catarrhini;
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                                                                     S., Yamazaki
Shibahara T.
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ibahara T., Ta
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                                                                     i M., Tashi
r., Tanaka
    databases
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anaka T.,
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Best Local
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                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
AXONEME-ASSOCIATED PROTEIN GASP-180.
Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardia
                                                                                                            Q962Q0
Q962Q0;
                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE
                Elmendorf
                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
Canis familiaris (Dog).
Chordata; Craniata; Vertebrata;
Craniata; Vertebrata; Cranidae;
                                          NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                EMBL; X87224;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-95310363; PubMed-7790375;
Wanker E.E., Sun Y., Savitz A.J., M
"Functional charcterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                 P180
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q28298
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                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                   Vivo.
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                                                                                                                                                                    QLQGKIRTLQEQLENGPNTQLARLQQENSIL
                                                                                                                                                                                      ELEGEITTLNHKLQDA-SAEVERLRRENQVL 144
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                                                                                                                                                                                                         DAAVAKSKLREVNKELAAEKAKAAAGEAKVKKQLVAREQEITAVQARIEASYREHVKEVQ 906
                                                                                                                                                                                                                            DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDSLHATAELLQVRVQSLTHILALQEEELTRKVQPSDSLEPEFTRKCQSLLNRWREKVFA
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26; Conser
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               H.G.,
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      A N.A.
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AA; 88643 MW;
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Last annotation updat
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Pred. No. 1.7;
32; Mismatches
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Pred. No. 4.5;
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Canis.
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RESULT
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RESULT
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                                                                                                                     Q9YHD5;
01-MAY-1999
01-MAY-1999
01-DEC-2001
Eukaryota;
Amphibia; E
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
MACROPHAGE GALACTOSE N-ACETYL-GALACTOSAMINE SPECI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1401
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                                                                           MYOSIN HEAVY MHC-4.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF400249; AAK91740.1; -.
SEQUENCE 1627 AA; 179270 MW; 021EED9763907DCC CRC64;
                                             Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2001) to the EMBL/GenBank/DDBJ EMBL; BC014811; AAH14811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (OCT-2001)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
mes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46
                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 LGIGILVLLIIVILGVPLIIFTIKANSEACRD--GLRAVMECRNVTHLLQQELTEAQKGF 81
                                                                                                                                                                                                                                                                                                                                          |::||:: |: ::|: |
DHVQQLRKDLKALTCQLANLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDVEAQAATCNHTVMALMASLDAEKAQGQ-----KKVEELEGEI----TTLNHKLQDAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRESAEALQDKLHALSDSRAADGDLQKLVEQLEKDLSGAKELVAERDATIDELKQRLRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASL-DA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                         QSLDSRADSFEKGISSLKVDVEDHRQELQAGRDLSQKVTSLESTLEKREQALKTDLSDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGLSLLLLVVVSVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKAQGQK-KVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165
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  : Metazoa; :
Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304
                                                                                                                     (TremBLrel. 10, Creat
(TremBLrel. 10, Last
(TremBLrel. 19, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                 (FRAGMENT).
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Rodentia;
                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.4%;
23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34622 MW;
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27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SQNSQLRRDLGTLRAILD--NTTSKIKAE-----F
     Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
  Neobatrachia; V
                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101.5;
Pred. No. 0.8
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Pred.
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                            -NNGSEVACCP 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2272E1ADA2C0262A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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No. 4.8;
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  Vertebrata;
a; Ranoidea;
                                                                                                                                                                                                                    AA
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SPECIFIC
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                                                                                                                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                         Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304;
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Best Local
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Best Local Similarity
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EMBL; AF097907; AAD13772.1; -.

InterPro; IFR002928; Myosin_tail.

InterPro; IFR000533; Tropomyosin.

pfam; pF01576; Myosin_tail; 1.

PRINTS; PR00194; TROPOMYOSIN.

NON_TER 1
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                                                                                                                                                                                                                    Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK00533; BAA91236.1;
SEQUENCE 506 AA; 57358 MW; B41ABD7DB1EFA495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CDNA FLJ20526 FIS, CLONE KAT10627.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Expression of the Myosin Heavy Chain Genes
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 128
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                         142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 KANSEACR------DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALM
                                                   89
                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSUE-TAIL MUSCLE, HINDLIMB MUSCLE;
H., Merrifield P., Atkinson B.G.;
                                                                                                     8
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                                                                                                                            RDGLRAVME-----CRNVTHLL---QQELTEAQKGFQDVEAQ-AATC-----NHTVMA
                        QVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMKNAYEEALEQVETLKRENKNLQQEISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEEQVEAVNSKCASLEKTKQRLQ 313
LQLELSRAQEARRRWQQQTAS-AEEQLRLVVNAVSS
                                                                        LMASLDAEKAQGQKKVEELEGEITTLNHK-------LQDASAE--VERLRREN 141
                                                                                                   RDSLHATAELLQVRVQSLTHILALQEEELTRKVQPSDSLEPEFTRKCQSLLNRWREKVFA
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                                                LMVQLKAQELEHSDSVKQLKGQVASLQEKVTSQSQEQAILQRSLQDKAAEVGVERMGAKG
                                                                                                                                                       41;
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26.3%;
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                                                                                                                                                     Score 100.5; D
Pred. No. 1.9;
29; Mismatches
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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 162
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Best Local
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InterPro; IPR001245; Tyr_pkinase.
Pfam; PP02185; HR1; 1.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
SMART; SM00074; HR1; 1.
SMART; SM00074; HR1; 1.
SMART; SM000720; S_TKC; 1.
SMART; SM00133; S_TKC; 1.
SMART; SM00133; S_TK_X; 1.
SMART; SM0019; TYRKC; 1.
SMART; SM0019; TYRKC; 1.
SMART; SM0019; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_TOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rivkees S.A., Schwartz R.J., Imanaka-Yoshida K
"Rho kinases play an obligatory role in verteb
organogenesis.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL; AF347075; AAK29627.1; --
                                                                                  P79391;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RNO-ASSOCIATED COLLED-COLL FORMING KINASE 1 (FRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98SN6
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Mammalia; Eutheria; Cetartiodactyla; Rur
                                               Bos taurus (Bovine).
                                                                        LECTIN-LIKE OXIDIZED LDL RECEPTOR.
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InterPro; IPR000961; Pkinase_C.
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L., Roberts W., Wang L., Yamada M., Zhang S.

Local S.A., Schwartz R.J., Imanaka-Yoshida K.;
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RA Sawamura T., Kume N., Aoyama T., Moriwaki H., Hoshikawa H., Aiba Y.,

RA Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T.;

RT "An endothelial receptor for oxidized low-density lipoprotein.";

RL Nature 386:73-77(1997).

DR EMBL; D89049; BAA19005.1; -.

DR HSSP; P20693; 1HLJ.

DR HSSP; P20693; 1HLJ.

DR InterPro; IPR001304; lectin_c.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM00034; CLECT; 1.

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KW Receptor.
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MYSP_ONCVO
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MYH6_MOUSE
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MYSS_RABIT
MYH6_RAT
MYH6_MESAU
MYSP_CAEEL
MYH7_PAPHA
FLT2_CARAU
MYSC_CHICK
MYH7_MESAU
MYH7_HUMAN
MYH7_RAT
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VDP_RAT
YM92_CAEEL
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8 papio hamad
6 carassius a
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IShikawa J., Kaisho T., Tomizawa H., Lee B.O., Kobune Y., Inazawa J., Oritani K., Itoh M., Ochi T., Ishihara K., Hirano T.; "Molecular cloning and chromosomal mapping of a bone marrow stromal cell surface gene, BST2, that may be involved in pre-B-cell growth."; Genomics 26:527-534(1995).

J. FUNCTION: MAY BE INVOLVED IN PRE-B-CELL GROWTH.

SEQUENCE FROM N.A.

MEDLINE=95331788;

PubMed=7607676;

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606;

<del>-</del> <del>-</del> <del>-</del> <del>-</del>

AND BRAIN.

SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER, LUNG,

AND PLACENTA. LOWER LEVELS IN PANCREAS, KIDNEY,

SKELETAL

MUSCLE

45	44	43	42	41	40	39	38	37	36	35	34
89	89.5	89.5	90	90	90.5	90.5	90.5	90.5	90.5	91	91
10.0	10.1	10.1	10.1	10.1	10.2	10.2	10.2	10.2	10.2	10.2	10.2
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						P12882 homo					
gallus gall	sapien	sapien	yosteli	musculu	us norv	sapien	us gall	us norv	coryne	enterococcu	streptococc

### ALIGNMENTS

RESULT 1 BST2\_HUMAN

BST2\_HUMAN Q10589;

STANDARD;

180 Ą

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bone marrow stromal antigen 2 (BST-2).

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Query Match
Best Local S
Matches 180
                                                                                       CARBOHYD
CARBOHYD
                                                                                                            TRANSMEM
DOMAIN
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                                                        SEQUENCE
                                                                                                                                  Transmembrane;
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                                                                                                                                                                   EMBL; D28137;
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                                                                             VARIANT
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100.0%; ilarity 100.0%; Conservative
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49
65
92
143
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                                                                                                                                             Glycoprotein;
                                                        AΑ;
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48
180
65
92
                                                      19769
                                                        MW;
                                                                           Signal-anchor; Polymorphism.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
V -> F (IN DBSNP:1804402).
                                                     V -> F (IN DBSNP:1804402).
/FTId=VAR_012067.
CAF52340D69061EE CRC64;
Score 889; DB 1;
Pred. No. 1.3e-63;
; Mismatches 0;
                     Length 180;
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Similarity

0;

Indels

0,

Gaps 60

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MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV

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RESULT
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01-APR-1990
16-OCT-2001
                                                                                                                                                                                                                                                             Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00503; SynN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE A COULD BE INVOLVED IN ENDOCYTOSIS.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: KUPFFER CELLS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 83-104.
MEDLINE-88227939; PubMed=2836387;
HOyle G.W., Hill R.L.;
"Molecular cloning and sequencing of a cDNA for binding receptor unique to rat Kupffer cells.";
J. Biol. Chem. 263:7487-7492(1988).
                                                                                                                                                                                                                     PROSITE; PS00615; C_TYPE_LECTIN_1; PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J03734; AAA41472.1; -. EMBL; M55532; AAA40892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Structure of the gene for a carbohydrate-binding rat Kupffer cells.";
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Mammalia; Eutheria;
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InterPro; IPR001304; lectin_c.
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A38674; A38674.
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                      (POTENTIAL).

EXTRACELLULAR (C-TYPE LECTIN (BY SIMILARITY.BY SIMILARITY.BY SIMILARITY.BY SIMILARITY.
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SIGNAL-ANCHOR
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OR (TYPE-II
                                                                   (SHORT FORM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=89196920; PubMed=2467843;
Ichinose Y., Morita T., Zhang F.,
Matsumoto M., Nozaki M., Matsushii
"Nucleotide sequence and structure
                   Genes Dev. 2
                                                                                        SEQUENCE OF 1-131 FROM N.A.
MEDLINE=88255838; PubMed=2454868;
Oshima R.G., Trevor K., Shevinsky L.H.,
"Identification of the gene coding for "
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-86085876; PubMed=2416755;
Singer P.A., Trevor K., Oshima R.G.;
"Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                       cytoskeletal protein induced during teratocarcinoma cells."; Roux's Arch. Dev. Biol. 196:16-21(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P05784; Q61766;
01-NOV-1988 (Rel. 09, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                         and its methylated,
                                                                                                                                                                                           expressed in preimplantation mouse J. Biol. Chem. 261:538-547(1986).
                                                                                                                                                                                                                                                                                                                                                             "ISSUE-reractoration.",
Alonso A., Weber T., Jorcano J.L.;
"Cloning and characterization of keratin D, a
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Teratocarcinoma; Alonso A., Weber T., Jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keratin, type I cytoskeletal 18 (Keratin D).
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                                                           cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 70:85-95(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRT18 OR KRT1-18 OR KERD
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                                       2:505-516(1988)
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8 ASSOCIATES WITH
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Nozaki M., Matsushiro
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Rodentia;
                                                                            stable
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9358A6CF4C306270 CRC64;
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 TWO TYPE
KERATIN 8
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No. 0.
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                                                                            mouse
                                                                                                                                                                                                                                                                                                                                                                   differentiation
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                       TWO
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                     II KERATINS
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PIR; A28428; A28428.
PIR; JT0406; JT0406.
SWISS 2DPAGE; P05784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:96692; Krt1-18.
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M22832; AAA37552.1; -. EMBL; M36376; AAA39373.1; -. EMBL; M11686; AAA39390.1; -. EMBL; Y00217; CAA68365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intermediate filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00038; filament;
                                              336
                                                                                           276
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SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL (40-55 AND 56-70 KILODALTONS, RESPECTIVELY).
                                                                                                                                                               VEAQAATCNHTV---
                                                                    GLSALL 179
                                                                                                                                                                                                           FTIKANSE-ACRD-
                                              HLESEL 341
                                                                                                                TLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSS-----SAAAPQLLIVLL
                                                                                       TKSAEIRDAETTLTELRRTLQTLEIDLDSMKNQNINLENSLGDVEARYKAQMEQLNGVLL
                                                                                                                                       LEAQIASSGLTVEVDAPKSQDLSKIMADIRAQYEALAQKNREELDKYWSQQIEESTTVVT
                                                                                                                                                                                    FRVKYETELAMRQSVESDIHGLRKVVDDTNITRLQLETEIEALKEELLEMKKNHEEEVQG
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR01248; TYPE1KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00226;
                                                                                                                                                                                                                                                                                           380
71
107
125
217
2241
263
323
323
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31
49
133
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242
422
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27.4%;
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                                                                                                                                                                                                                                   27;
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STUTTER.
O-LINKED (GLCNAC)
O-LINKED (GLCNAC)
O-LINKED (GLCNAC)
                                                                                                                                                                                                                                 Score 101; DB
Pred. No. 0.51
?7; Mismatches
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LINKER 1.
COIL 1B.
LINKER 12.
COIL 2.
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N (IN REF. 2).
G (IN REF. 2).
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                                                                                                                                                              121
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Q

24

LGIGILVLLIIVILGVPLIIFTIKANSEACRD--GLRAVMECRNVTHLLQQELTEAQKGF 81

Query Match Best Local S Matches 36

l Similarity 36; Conserv

Conservative

37;

Score 99.5; D. Pred. No. 0.47 37; Mismatches

99.5; No. 0.

DB.47;

Length Indels

49; 1;

33;

Gaps

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11.2%; 23.2%;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage agalactose/N-acetylgalactosamine-specific lectin) (MMGL).
                                                                                                                                                                                                                                                                                                                                                                   EMBL; S36676; AAB22171.1; -. HSSP; P06734; 1KJE. MGD; MGI:96975; Mg1. InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalactosamine-specific lectin on mouse tumoricidal macrophages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biochem. 111:331-336(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C3H/HEN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P49300;
01-FEB-1996
                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C3H/HEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 102-120 AND 137-151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato M., Kawakamyi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMGL_MOUSE
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                            PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92268032;
                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                          Lectin; Glycoprotein;
DOMAIN 1 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MACKUPHANDE ....
SUBUNIT: HOMO-OLIGOMER.
SUBCELLULAR LOCATION: Type II membrane p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECOGNIZES TERMINAL UNITS. MAY PARTICIPATE IN THE MACROPHAGES AND TUMOR CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MACROPHAGES.
                                                                       57
172
173
201
274
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       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=1587794;
304
298
184
296
288
74
166
34596
                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osawa T.,
       WW;
  (POTENTIAL).

EXTRACELLULAR (POTENT EXTRACELLULAR (POTENT EXTRACELLULARITY.

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N-LINKED (GLCNAC. OF THE EXTRACE. OF THE EXTRACE OF THE EXACT OF THE EXTRACE OF THE EXTR
                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                   CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALACTOSE AN INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 T.;
sf a lectin-like molecule specific
sf from tumoricidal macrophages.";
                                                                                                                                                                                                                                   Calcium; Signal-anchor.
SMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e protein.
E SURFACE
                                                                                                                                       (POTENTIAL). (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND N-ACETYLGALACTOSAMINE ON BETWEEN TUMORICIDAL
       CRC64;
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                                                 (POTENTIAL)
                            (POTENTIAL)
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tent is in
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MBL outstation –
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MUTAGEN
SEQUENCE
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060763;
                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There \tilde{\epsilon}
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sohda M., Misumi Y., Yano A., Takami N., Ikehara "Phosphorylation of the vesicle docking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., MEDLINE=98148093; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pl15 (Transcytosis associated
                                                                                                                                Transport;
                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein) (TAP) (Vesicle docking protein).
VDP.
                                                                                      DOMAIN
                                                                                                  DOMAIN
                                                                                                            DOMAIN
                                                                                                                      Phosphorylation
                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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               y Match
Local !
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                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                603344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSLDSRADSFEKGISSLKVDVEDHRQELQAGRDLSQKVTSLESTVEKREQALKTDLSDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDVEAQAATCNHTVMALMASLDAEKAQGQ.----KKVEELEGEI----TTLNHKLQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGLSLLLLVVVSVIG------SQNSQLRRDLGTLRATLD--NTTSKIKAE-
                                                                                                                                                                        D86326; BAA25300.1;
                Similarity
                                                                                                                                PS50176; ARM_REPEAT;
t; Protein transport;
                                                                                                                                                     IPR000225; Armadillo.
                                                                638
935
942
942
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930
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                                                          107906
                11
28
               . 18;
                                                          W.
               Score
Pred.
                                                       PHOSPHORYLATION.
S->A: LOSS OF PHOSPHORYLATION
Z: 2E748F2C1BC2B942 CRC64;
                                                                                     COILED COIL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
                                                                                                           GLOBULAR HEAD
                                                                                                                                Golgi stack;
                                                                                                                                         UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
               99;
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                                                                                                                                                                                                                      There are no rest
                . DB
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                        1;
                                                                                                                                Membrane;
                         Length 962
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                                                                                                                                Coiled
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21-JUL-1986
16-OCT-2001
                                                                                                                                                                                                                                                          -I- FUNCTION: MÜSCLE MYCSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-I- SUBUNIT: MUSCLE MYCSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-I- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
-I- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITUE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McLachlan A.D., Karn J.;
"Periodic charge distributions
"periodic charge distributions in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=83273600; PubMed=6576334;
Karn J., Brenner S., Barnett L.;
"Protein structural domains in the Caenorhabditis elegans unc-54
myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                         "The genes sup-7 X and sup-5 III of C. e nonsense mutations via altered transfer Cell 33:575-583(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1876-1966 FROM N.A. MEDLINE=83232892; PubMed=6571695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin heavy chain B (MHC B). UNC-54 OR MYO-4.
                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wills N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83232892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          match cross-bridge spacings Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=82272395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 850-1966 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
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                                                           WALL MUSCLE. THEY CO-
SIMILARITY: CONTAINS
                                                                                                                                                        CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ACT SELECTIVELY

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                           MISCELLANEOUS: MHC A AND MHC B ARE WALL MUSCLE. THEY CO-ASSEMBLE INTO SIMILARITY: CONTAINS 1 MYOSIN-LIKE
                                                                                                                             MISCELLANEOUS:
                                                                                                                                               SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ž17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEELKRNQELLQSQLTEKDSMIENMKSSQTSGTNEQSSAIVSARDSE------QVAELKQ 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gesteland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        966 FROM N.A.
PubMed=7202124;
                                                                                                                             THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                          R.F., Karn J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the muscle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Barnett L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1966 AA.
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                                                                             BODY WALL
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er RNA.";
                                                                GLOBULAR HEAD DOMAIN
                                                                               EXCLUSIVELY IN THE WALL THICK FILAMENT
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MYH4_R

MYH4_R

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DT 16-OCT
DT 16-OCT
DC OCYCTO
OC CURATY
OC WATMAL

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RP SEQUEN
RC STRAIN
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RA Mittin
RI "Isola
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Best Local :
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                            Q28641;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, juvenile.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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CONFLICT
SEQUENCE
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DOMAIN
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MOD_RES
                                                                                                                                                                                                                   1928
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 "Isolation, sequencing of myosin heavy chain co
skeletal muscle and a novel cosynthesis of S-1
essential and regulatory light chains.";
                                      STRAIN-NEW ZEALAND Waeda K., Hostinova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00063; myosin_head; 1. Pfam; PF02736; Myosin_N; 1. Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J01050; AAA28124.1; -. EMBL; V01494; CAA24738.1; -. PIR; A02992; MWKW.
                             Wittinghofer A.;
                                                          SEQUENCE FROM
                                                                                                                                                                    MYH4_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P08799; 1MND
                                                                                                                                                                                                                                      142 QVLSVRI---ADKKYYPSSQDSSSAA 164
                                                                                                                                                                                                                                                                              107
                                                                                                                                                                                                                                                                                                                  47 KANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEK 106
                                                                                                                                                                                                                    SLSKMRSKSRASASVAPGLQSSASAA 1953
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705
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1337
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                                                          N.A.
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                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                               11.1%; 24.7%;
                                    Z; TISSUE=Skeletal muscle;
Roesch-Kleinkauf A., Schuster H.,
                                                                                                                                                                                                                                                                            -GQKKVEELEGEITTLN------HKLQDASAEVERLRREN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alkylation;
                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                 ALKYLATION
ALKYLATION
E -> R (IN I
I -> L (IN I
                                                                                                                                                                                                                                                                                                                                                Score 98.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGHT MEROMYOSIN (LMM).
ATP (BY SIMILARITY).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA-HELICAL TAILPIECE
                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coil; Thick filament; Ac
lation; Multigene family.
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      > R (IN REF. 2).
> L (IN REF. 2).
B66F0BB2FE27B67F CRC64;
                                                                                                                                                                    1938
                                                                                                                                                                                                                                                                                                                                                                                                                  (SH-1)
(SH-2)
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                  cDNA from rabbit
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SEQUENCE
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SMART; SM00242; MYSc; 1.
PROSITE; PS50096; IQ; 1.
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                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000355;
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a
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                                                                                                                                                                                                                                                                                                         Multigene
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                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                  Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                            139
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                                                                                                         KANSEACR-----
         KESRSLSTEVFKVKNAYEESLD
                                                                                                                                                                                                                                                                                                                                                                                      PF02736;
PF01576;
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                         family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000048; IQ
                                                                                                                                                                            1938
                                                                                                                            Conservative
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658
760
35
130
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813
1938
186
680
774
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-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases. -i- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32574; AAA74199.1; -. HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LA SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 RO SUBERAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS ($1) AND 1 ROD-SHAPED
                                                                                                                                                               KANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAE---EHVEAVNAKC------
RENQVLSVRIAD-KKYYPSSQD 159
                                                                                                          ASIDAEKAQGQKKVEELEGEITTLN----
                                                     ASLEKTKQRLQNEVEDLMIDVERTNAACAALDKKQRNFDKILAEWKHKYEETHAELEASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF000612; IQ; 2.
PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR004009; Myosin_N.
IPR002928; Myosin_tail.
IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin_N; 1.
Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myosin_head;
                                                                                                                                                                                                              -DGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                11.0%;
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ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (MONO-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

ALKYLATION (SH-1) (BY SIMILARITY).

ALKYLATION (SH-2) (BY SIMILARITY).

ALKYLATION (SH-2) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                             Score
Pred.
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COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                             No.
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4.6;
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                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                         Length 1938;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                          -HKLQDASAEVERLR
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MYSD_CA
ID MXSD_CA
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EMBL;
EMBL;
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21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Myosin heavy chain D (MHC D).
                                                                                                                                                                                        use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See I
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Karn J., Dibb N.J., Miller D.M.; "Cloning nematode myosin genes."; Cell Muscle Motil. 6:185-237(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karn J., Brenner S., Barnett L.;

"Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy chain gene are not separated by introns.";

Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89178677; PubMed-2926820;
Dibb N.J., Maruyama I.N., Krause M.
"Sequence analysis of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                              +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gardner A., McMurray
Submitted (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BRISTOL N2;
MEDLINE=89178677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=85201409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=83273600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 34-1795 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROMYOSIN (LMM) AND 1 HEAVY MESPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENT (S2).
                              X08065; CAA30854.1;

X087232; AAA28119.1;

X087234; AAA28120.1;

X17266; CAA95848.1;

X71261; CAA95848.1;

X71261; CAA95848.1;

X71261; CAA95848.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain gene family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=3888374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=6576334;
                                                      JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Karn J.;
Caenorhabditis elegans myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1938
                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
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RESULT 9
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Best Local S
Matches 34
                                                                          01-AUG-1991
01-AUG-1991
16-OCT-2001
PUFF II/9-2
                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
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CONFLICT
CONFLICT
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CONFLICT
                            Pterygota;
Sciaridae;
                                                                                                                                                                                                                   1384
                                                                                                                                                                                                                                                       1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE FROM N.A
                  NCBI_TaxID=38358
                                              Eukaryota;
                                                        Sciara coprophila (Fungus
                                                                                                                                                                            1439 VDRHLTVI 1446
                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                  11/9-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z71266; CAA(
PIR; S02772; MWKWJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001609; myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004009; Myosin_N
InterPro; IPR002928; Myosin_ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WormPep; R06C7.10
                                                                                                                                                                                              164 AAPQLLIV 171
                                                                                                                                                                                                                                     104
                                                                                                                                                                                                                                                                        51 EACRDGLRAVME----CRNVTHLLQQ--ELTEAQ-KGFQDVEAQAATCNHTVMALMASLD 103
                                                                                                                                                                                                                  GEGLVGSEELEELKRKQMNRVMDLQEALSAA-----QNKVISLEKAKGKLLAETEDARSD 1438
                                                                                                                                                                                                                                    AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSA 163
                                                                                                                                                                                                                                                       KAAEDELHERQEFHAACKNLEHELDQCHELLEEQINGKDDIQRQLSRINSEISQWKARYE 1383
                                                                                                                            scico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF02736; Myosin_N; 1. PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00063; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P08799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                    Similarity
                                              ophila (Fungus gnat).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                     Neoptera;
                                                                          protein precursor
                                                                                   (Rel. 19, Created)
(Rel. 19, Last sequence up)
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                      389
391
408
474
577
681
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAA95806.1; JOINED
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                     1659
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1938
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1170
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710
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98
377
390
391
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474
577
681
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682
778
128
                                     Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                    11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin_tail
                                                                                                                                                                                                                                                                                                                                           223255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alkylation; Multigene family. MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                         DV -> GD (IN REF. 2).
V -> D (IN REF. 4).
W -> N (IN REF. 2).
Q -> G (IN REF. 2).
L -> F (IN REF. 4).
I -> N (IN REF. 4).
I -> N (IN REF. 4).
S -> D (IN REF. 3).
E -> Q (IN REF. 3).
                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                          Score 98; DB
Pred. No. 4.6;
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         A ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHYLATION (TRI-).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                 V -> D
                                                                                                                                                                                                                                                                                                                                                                                                                                                   F -> E (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGHT MEROMYOSIN (LMM).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RODLIKE TAIL (S2 AND LMM DOMAINS). ALPHA-HELICAL TAILPIECE (SHORT S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                           387399C8F63A4CF4
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                                                                                                                            286
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                                                                                                                                                                                                                                                                                                                                                                                                                                        REF.
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                                                                                                                                                                                                                                                                                                              1;
                                      Nematocera;
                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                             Length 1938;
                                                                                                                                                                                                                                                                                                                                                                                                                      2).
                                                                                                                                                                                                                                                                                                                                           CRC64;
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                                      Sciaroidea
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Best Local
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PTR; S07533; POILE
                                                                                                                                                                                                                                                VDP_RAT
P41542;
                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pli5 (Transcytosis associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; 
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Coiled
                                                                                                                                                                                         protein) (TAP) (Vesicle docking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coprophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dibartolomeis S.M., Gerbi S.A.; "Molecular characterization of DNA puff II/9A genes in
TISSUE-Liver;
          SEQUENCE FROM
                                          endoplasmic
                                                                 Waters M.G.;
                                                                           Sapperstein S.K.,
                                                                                      MEDLINE=95132632;
                                                                                                   TISSUE-Liver;
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=10116
                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90133907; PubMed=2614832;
                                                     "p115 is a general vesicular transport factor related
                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                                                                                                                                                                                  143
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                                                                                                                                                                                                                                                                                    10
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                                                                                                                                                                                                                                                                                                                     æ
                                                                                                                                                                                                                                                                                                                                          æ
                                                                                                                                                                                                                                                                                                                                                               ----KENAKILNKIEELNCTITQLQEKLERCRGRERDLQCQLDECKKKLNICNNELIAC 197
                                                                                                                                                                                                                                                                                                                                                                                                             LKREKEARQKAEKALKECQKNTENLKETIEQLKKELAEAQKALEKCKKELADCK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  IKANSEACRDGLRAVMEC-RNVTHL-----LQQELTEAQKGFQDVEAQAATCNHTVMAL 98
                                                                                                                                                                                                                                                                                                                                                                                      MASLDAEKAQGQKKVEELEGEITTLNHKLQ------DASAEVERLRRE-----NQVLSV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               x51679;
                                 Natl.
                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                              Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
20
61
156
286
                                reticulum
Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S07533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAA35982.1; -.
          N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coil; Glycoprotein.

1 19 OR 21 (POTENTIAL).

0 286 PUFF II/9-2 PROTEIN.

1 235 HELICAL (POTENTIAL).

1 235 HELICAL (GLCNAC...

6 156 N-LINKED (GLCNAC...

AA; 32621 MW; 720AC8CCC22A869C CF
                                                                                                                                                                                                                                                             STANDARD;
                                                                             Walter
                                                                                       PubMed=7831323;
          AND PARTIAL SEQUENCE
                                                                                                                                              Rodentia;
                                                                                                                                                          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.9%;
                                to Golgi
                                                                          D.M., Grosvenor A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                              i transport factor
92:522-526(1995).
                                                                                                                                             Sciurognathi;
                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  720AC8CCC22A869C CRC64;
                                                                                                                                                                                          protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.
                                                                                                                                                                                                                                                             959
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                                                                                                                                                                                                                                                             AA.
                                          factor Usolp.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                              Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                          Heuser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                             Murinae; Rattus.
                                                      ţ
                                                                          J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
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                                                     the yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 11
YM92_CAEEL S:
ID YM92_CAEEL S:
AC P34531; P34532; I
DT 01-FEB-1994 (Rel
DT 01-MAR-2002 (Rel
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Best Local
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CONFLICT
CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barroso M., Nelson D.S., Sztul E.;
"Transcytosis-associated protein (TAP)/pll5 is a general fusion factor required for binding of vesicles to acceptor membranes.";
Proc. Natl. Acad. Sci. U.S.A. 92:527-531(1995).

-! FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR INTERCISTENNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR AND TARGET MEMBRANES IN PROXIMITY.

-! SUBUNIT: HOMODIMER WITH TWO N-TERMINAL HEADS AND A C-TERMINAL SUBUNIT: HOMODIMER WITH TWO N-TERMINAL HEADS AND A C-TERMINAL COLLED-COIL TAIL. DIMER FORMED BY PARALLEL ASSOCIATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES
BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE.
-!- DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILED-COIL) AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.
-!- PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER;
PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U14192; AAA62632.1; EMBL; U15589; AAC52151.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95132633; PubMed=7831324;
                                                                                                                                         853
                                                                                                                                                                        178
                                                                                                                                                                                                     793
                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                  739
                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION PROMOSTES DISSOCIATION (BY SIMILARITY). SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE;
                                                                                                                                         LLQ 855
                                                                                                                                                                                                                                                                                              VMECRNVTHLLQQELTEAQKGFQDV-EAQAATCNHTVMALMASLDAEKAQGQKKVEELEG 118
                                                                                                                                                                        LLQ 180
                                                                                                                                                                                                                     EITTLNHKLQDASAEVERLRRENQVLSVRIAD-KKYYPSSQDSSSAAAPQLLIVLLGLSA
                                                                                                                                                                                                                                                                  IEELRSHQVLLQSQLAEKDTVIENLRSSQVSGMSEQALATCSPRDAE----
                                                                                                                                                                                                     ELSALKSQLCSQSLEITRLQTENSELQQRAETLAKSVPVEGESELVTAAKTTDVEGRLSA
                                                                                                                                                                                                                                                                                                                            Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50176; ARM_REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
532; P34533;

(Rel. 28, Created)

(Rel. 33, Last sequence update)

(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         638
935
940
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658
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873
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                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         637
930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport;
                                                                                                                                                                                                                                                                                                                                             10.9%;
30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                        107162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Armadillo.
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                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL).

ASP/GLU-RICH (ACIDIC).

PHOSPHORULATION (BY SIMILA
S -> P (IN REF. 2).
M -> V (IN REF. 2).
S -> R (IN REF. 2).
A -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                         Score 97; DB:
Pred. No. 2.6;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLOBULAR HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Golgi stack;
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                                                                                                                                                                                                                                                                                                                                                        97;
                                                             893
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                                                                                                                                                                                                                                                                                                                                                         Length 959
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restrictions on
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protein M01A8.2 in chromosome

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RESULT PU91_SC ID PU AC P2 DT 01 DT 11 DT 11
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Best Local
                    PU91_SCICO
P22311;
01-AUG-1991
01-AUG-1991
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; CDOMAIN 39 81
DOMAIN 522 696
DOMAIN 729 756
SEQUENCE 893 AA; 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Coraxton M., Dear S., Du Z., Dubin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Sounders D., Shownkeen I.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                SCICO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormPep; M01A8.2; CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BRISTOL N2;
MEDLINE=94150718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical 100.0 M01A8.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR000938; CAP-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                      685
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MOIAB.,

O; IPRO00938; C.,

O; IPRO00938; C.,

PFOL302; CAP_GLY; 1.

TE; PS00845; CAP_GLY_1; 1.

ITE; PS50245; CAP_GLY_2; 1.

CAP-GLY_2; 1.

CAP-GLY.

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

Len

Len
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$40999; $40999.
                                                                                                                                                                                ENQVLSVRI 148
                                                                                                                                                                                                                                                                    SNQQVIRNHANAV-ESLQKTHETQIAEKNKEFERNFEEERARREAEVCAMNNRHQKVVAC
                                                                                                                                                                                                                                                                                              ANSEACRDGLRAVMECRNVTHLLQ - - QELTEAQKGFQDV - - - - EAQAATCNHTVMALMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mb of contiguous nucleotide sequence
                                                                                                                                                      KNQNLSLQV
                                                                                                                                                                                                             LDEKISEAEKQCEQLNVDKKVLQAALANDCDHRNQMLTKEISSLQTALEMKSAEMKELRQ
                                                                                                                                                                                                                                      LDAEKAQGQKKVEELE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z27081; CAA81607.1;
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requires a license agreement (See http://www.isb-sib.ch/announce/
                      (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peloderinae;
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                                                                                STANDARD;
                       19,
19,
40,
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                                                                                                                                                                                                                                                                                                                                        10.9%;
                       Last
Last
                                                    Created)
                       sequence u
annotation
                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                PRT;
                                                                                                                                                                                                                                                                                                                           red. No. 2.6;
Mismatches
                       update)
on update)
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                                                                                                                                                                                                                                       -GEITTLNHKLQDASAEVERLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome III of
                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                       893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ω
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                                                                                                                                                                                                                                    RESULT 13
MYH8_HUMAN
                                                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
encoding
Gene 89:2
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities
or send a
                                                                                                                                                                    MYH8_HUMAN STANDARD; PRT; 19
P13535; Q14910;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular characterization of coprophila.";
                                 SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-90323631; PubMed-2373371;
Karsch-Mizrachi I., Feghali R., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 II/9-1.
Sciara coprophila (Fungus gnat).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Mematocera; Sciaroidea;
                                                                                                            Mammalia; Eutheria;
                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                          Myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11/9-1
                     "Generation of a full-length human
                                                                                              NCBI_TaxID=9606;
                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90133907; PubMed=2614832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=38358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUFF II/9-1 protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                     158
                                                                                                                                                                                                                                                                                                             119 EITTLNHKLQDASAEVERLR
                                                                                                                                                                                                                                                                                                                                      102 ALCECQKNSELLKQTIEQLKKELAQTKQELANCKEA----LANCKAENAKLLKKIEELNC 157
                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUI
D OF THE HEPTAD REPEAT.
SIMILARITY: 76% IDENTICAL TO THE PUFF II/9-2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THE DNA PUFF II/9 PROTEINS HAVE A PROPOSINTERMOLECULAR COILED COIL STRUCTURE WITH POSSIBLY INTEDISULFIDE BRIDGES FORMED BY NUMEROUS CYSTEINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S07532;
                                                                                                                                                                                                                                                                                   TITOLOEELEOCRARERDLO 177
                                                                                                                                                                                                                                                                                                                                                           AVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      x51680; CAA35983.1;
s07532; s07532.
                                                                                                                                                          heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. 210:531-540(1989)
         CDNA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
61
156
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                          il; Glycoprotein.

19 OR 21 (POTENTIAL).

286 PUFF II/9-1 PROTEIN.

235 HELICAL (POTENTIAL).

156 N-LINKED (GLCNAC. . .)

1, 32034 MM; AA6A7B55F191BB1D CRC
                                                                                                        Chordata;
Primates;
                                                                                                                                                          skeletal muscle,
                                                                                                                                                                                                                                                                                                                                                                                              10.8%;
                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                Score 96; DB 1 Pred. No. 0.84;
                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AA6A7B55F191BB1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                  Shows T.B.
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                       perinatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                puff II/9A
                                                                                                                                                                                                                        1937
                                                                                                                                                                                   update)
                                                                                                                                                          perinatal
                                                                                                                                                                       update)
                                                                                                            Hominidae;
                       Jr., Lein
al myosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAVE A PROPOSED POSSIBLY INTERMOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes
                                                                                                                                                          (MyHC-perinatal).
                                                                                                                                                                                                                                                                                                                                                                                                           Length 286
                                  Leinwand L.A.;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                        heavy-chain-
                                                                                                                       Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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RP SEQUENCE OF 1-46 FROM N.A.

RI SUBMITTED AND A CHARACTERISTS OF 1.1 SUBMITTED AND A CONSISTS OF 2.1 SUBMITTED AND A CONSISTS OF 2.2 ALKALI LIGHT CHAIN SUBMITS (MLC), 2 ALKALI LIGHT CHAIN SUBMITS (MLC)

CC HEAVY CHAIN SUBMITS (MC), 2 ALKALI LIGHT CHAIN SUBMITS (MLC)

CC AND 2 REGULATORY LIGHT CHAIN SUBMITS (MLC-2).

CC AND 2 REGULATORY LIGHT CHAIN SUBMITS (MLC-2).

CC I-1 SUBCELLULAR LOCATION: Thick filaments of the myofibrils. SHOWING CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CC CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

CC I-PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT CRAIN CAN BE SPLIT INTO 1 LIGHT CAN BE SPLIT INT
HSSP;
                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arnold H.H.;
"Identification of three developmentally controlled isoforms of human myosin heavy chains.";
Eur. J. Biochem. 189:55-65(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jullian E.H., Kelly A.M., Pompidou A.J. Stedman H.H., Rubinstein N.A.; "Characterization of a human perinatal transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human perinatal myosin heavy chain.";
J. Cell Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feghali R., Leinwand L.A.;
"Molecular genetic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 860-1937 FROM N.A. MEDLINE=89234168; PubMed=2715179;
                   PRINTS;
                                                                                                      InterPro; IF Pfam; PF0061
                                                                                                                                                                                                            MIM; 160741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bober E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90235862; PubMed=1691980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 502-1937 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95324556; PubMed=7601129;
                                                                                                                                           InterPro;
                                                                                                                                                              InterPro;
                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPLIT FURTHER INTO 2 SUBFRAGMENT (S2).
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                                       PF02736;
PF01576;
                                                                                                                                                                                                                                                                                      M36769; AAC17185.1; -. Z38133; CAA86293.1; -. X51592; CAA35941.1; -. M35250; AAA36346.1; -.
                                                                                                                                                                                                                             P08799; 1LVK.
                                                                                                                                                                                                                                                                       AF067143; AAC21557.1; -.
PD000355; myosin_head; 1.
                                                                                                                     IPR004009; | IPR002928; | IPR001609; |
                                                                                                                                                                                      IPR000048;
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                                                                                                 iQ;
                                    Myosin_N; 1.
Myosin_tail; 1.
                                                                                myosin_head; 1.
                     MYOSINHEAVY
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                                                                                                                   Myosin_N.
Myosin_tail.
myosin_head.
                                                                                                                                                                                    IQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
titute. There
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                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled coil; Thick filament;
Myosin; Muscle protein; Alkylation; Multigene famil
                             Genomics [2]
                                            MEDLINE=99425270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA shuman chromosome 16p and 16q.";
                                                                                                                                                                                     MYHB_HUMAN STANDARD: PRT; 1972 AA. P35749; 000396; P78422; 094944; 01-JUN-1994 (Rel. 29, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Myosin heavy chain, smooth muscle isoform (SM
                                                                                                                                                                                                                                                                                        1486
                                                                                                                                                                                                                                                                                                                               1426
                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                             MYH11 OR KIAA0866
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                 SEQUENCE OF 1-1266 FROM N.A
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=9606;
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                                     60:295-308(1999).
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                                                                                                                                              Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%;
25.2%;
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                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                    isoform (SMMHC).
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7.9;
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family;
                                                       of DNA sequence
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4;

MEDLINE=99156230; PubMed=10048485;

TISSUE=Brain;

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Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 2.
SMART; SM000242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED AND USCLE CONTRACTION.

-II FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-II SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-II SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-II SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-II TISSUE SPECIFICITY: SMOOTH MUSCLE; EXPRESSED IN THE UMBILICAL ARTERY, BLADDER, ESOCHAGUS AND TRACHEA.

-II DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

-II PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-II DISBASE: A CHROMOSOMAL REARRANCEMENT, KNOWN AS PERICENTRIC INVERSION INV(16)(P13Q22), PRODUCES A FUSION PROTEIN THAT CONSISTS OF THE 165 N-TERMINAL RESIDUES OF CBF-BETA (PEPB2) WITH THE TAIL REGION OF MYHILL THIS REARRANCEMENT, KNOWN AS PERICENTRIC REGION OF MYHILL THIS REARRANGEMENT IS ASSOCIATED WITH ACUTE MYELOID LEUKEMIA OF M4EO SUBTYPE.

-I MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation; Multigene family; Proto-oncogene; Chromosomal translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 885-1972 FROM N.A. MEDLINE-93263189; PubMed-7684189; Matsuoka R., Yoshida M.C., Furutani Y., Yanagisawa M., Masaki T., Takao A.; "Human smooth muscle myosin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
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                                                                                   PROSITE; PS50096; IQ;
                                                                                                                                                                                                                                                                                                                          InterPro; IPR002928;
InterPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P08799
MIM; 160745;
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                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 MYOSIN-LIK SIMILARITY: CONTAINS 1 IQ DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF001548; AAC31665.1; -. U91323; AAC35212.1; -. AB020673; BAA74889.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 D10667; -; NOT_ANNOTATED_CDS
X69292; CAA49154.1; -.
P08799; 1MMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16q12.";
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5:355-364(1998).
                                                                                                                                                                                                                                                                                                    IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                  IPR000048;
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                                                                                                                                                                                                                                                                                              Spectrin.
myosin_head
                                                                                                                                                                                                                                                                                                                                                      Myosin_tail.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

European

Bioinformatics

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Best Local
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CONFLICT
                                                                                              -!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-!- SUBCELLULAR SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
                                                                                                                                                                                                                                                       Proc.
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                            MYH11
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 CRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLD---
                                              MEROMYOSIN (LMM) AND 1 HEAVY MEROMY SPLIT FURTHER INTO 2 GLOBULAR SUBFR SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
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                                                                                                                                                                                                                                                      ' end of the gene.";
Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                               complete nucleotide and protein coding sequence
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
hitheria; Lagomorpha; Leporidae; Oryctolagus.
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786 815
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(Rel. 33, Last sequence update)
(Rel. 40, Last annotation updat
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24.5%;
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ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
EEK -> NSE (IN REF. 3).
ELQS -> TI-SF (IN REF. 2).
TI-> S (IN REF. 3).
KQ -> NE (IN REF. 3).
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Pred. No.
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T -> L (IN REF. 3).
WW; 67665BB2AECE1277
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RICETPRO; IPRO02928; Myosin_tail.

RICETPRO; IPRO02928; Myosin_tail.

RICETPRO; IPRO02017; Spectrin.

RICETPRO; IPRO02018; Spectrin.

RICETPRO; IPRO02018; Spectrin.

RICETPRO; IPRO02018; Myosin_head; 1.

RICETPRO; IPRO02018; Myosin_head; 1.

RICETPROSITE; PRO01035; Myosin_head; 1.

RICETPROSITE; PS00042; MYOSIN_head; 1.

RICETPROSITE; PS00041; ATP-binding; Methylation; Alkylation; Multigene family.

THE DOMAIN 785 807 IQ.

BOMAIN 785 807 IQ.

BOMAIN 1935 1972 ATP COILED COIL (POTENTIAL).

BOMAIN 1935 1972 ATP COTENTIAL.
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Best Local Similarity 24.5%;
Matches 27; Conservative 1
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                                                                                1328 TROKLNYSTKLROLEDERNSLOEQLDEEMEAKONLERHISTLNIQLSDSK 1377
                                                                                                                                                1268 CSDGERARAELNDKVHKLQNEVESVTGMLSEAEGKAIKLAKEVASLGSQLQDTQELLQEE 1327
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                                                                                                                 104 -AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKK 152
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              2002, 18:44:50
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s; Pred. No. 8;
18; Mismatches
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10.

COILED COIL (POTENTIAL).
CARBOXYL-TERMINAL.
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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Post-processing: Minimum Match 0% Maximum Match 10
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C;Genetics:
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A; Residues: 1-180 <ISH>
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Best Local Sim
Matches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type: DNA
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Result No.

Score

102.5 102 108 107.5 107

99 98.5 99.5

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96.5 96.5 96

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10.3	10.3	10.3	10.3	.10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.4	10.4	10.4	10.4	10.5
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centrosome associa	myosin alpha heavy	myosin beta heavy	myosin beta heavy	myosin heavy chain	myosin heavy chain	myosin heavy chain	beta-myosin heavy	hypothetical prote	paramyosin - Caeno	myosin II heavy ch	alpha cardiac myos	myosin heavy chain	general stress pro	secreted 45 kd pro	smooth muscle myos

### ALIGNMENTS

C;Species: Homo Sapiens (man)
C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 21-Jul-2000
C;Accession: A56836
R;Ishikawa, J; Kaisho, T; Tomizawa, H; Lee, B.O.; Kobune, Y.; Inazawa, J.; Oritani Genomics 26, 527-534, 1995
A;Title: Molecular cloning and chromosomal mapping of a bone marrow stromal cell surf A;Accession: A56836
A;Accession: A56836
A;Status: preliminary; not compared with conceptual translation hypothetical protein ORF82 - Lymantria dispar nuclear polyhedrosis virus C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999 C;Accession: T30430 R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, Virology 253, 17-34, 1999 A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for LA;Accession: T30430 A;Accession: T30430 A;Status: preliminar; translated from GB/EMBL/DDBJ A;Cross-references: GDB:409946; OI A;Map position: 19p13.2-19p13.2 C;Keywords: transmembrane protein 1 MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV ilarity 100.0%; Conservative GB:D28137; NID:g457563; PIDN:BAA05679.1; PID:g506861 100.0%; OMIM:600534 ; Score 889; DB 2; ; Pred. No. 2.6e-62; 0; Mismatches 0; baculovirus pathogenic for Lymantri Length 180; Indels 0; Gaps 180 60 60 0 J.M.;

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                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA A; Residues: 1-133, F', 135-243, D', 245-252, A', 254-423 <ICH>A; Cross-references: GB:M22832; NID:g340757; PIDN:AAA37552.1; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tricross-references: GB:Y00217; NID:g50842; PIDN:CAA68365.1; R;Ichinose, Y; Morita, T.; Zhang, F.; Srimahasongcram, S.; Gene 70, 85-95, 1988
A;Title: Nucleotide sequence and structure of the mouse cyto A;Reference number: JT0406; MUID:89196920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-243, D; 245-252, 'A', 254-423 <SIN>
A;Residues: 1-243, D; 245-252, 'A', 254-423 <SIN>
A;Cross references: GB:M11686; NID:9198620; PIDN:AAA39390.1; PID:9293685
A;Coshima, R.G.; Trevor, K.; Shevinsky, L.H.; Ryder, O.A.; Cecena, G.
Genes Dev. 2, 505-516, 1988
A;Title: Identification of the gene coding for the endo B murine cytoker.
A;Title: Identification of the gene coding for the endo B murine cytoker.
A;Reference number: A28428; MUID:88255838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M36376; NID:g198587; PIDN:AAA39373.1; PID:g293682 R;Singer, P.A.; Trevor, K.; Oshima, R.G. J. Biol. Chem. 261, 538-547, 1986

A;Title: Molecular cloning and characterization of the endo B cytokerati A;Reference number: A25621; MUID:86085876

A;Accession: A25621
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                                                                                                                                                                                                                                                                                                                                                              A; Gene: endoB; KERD
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A; Residues: 1-423 <RES>
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Roux's Arch. Dev. Biol. 196, 16-21, 1987
A;Title: Cloning and characterization of keratin D,
A;Reference number: 159463
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A;Cross-references: EMBL:AF081810; PIDN:AAC70268.1
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Best Local Similarity 32.5
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Residues: 1-132 <OSH>
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       84 VEAQAATCNHTV-
                                                                                                        44 FTIKANSE-ACRD-----
                                                                                                                                                                                  Local Similarity
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                                                                                                                                                       Conservative
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                                                                                                   -GLRAVMECRNVTHL------LQQELTEAQKG----FQD
     -MALMASIDAE-KAQGQKKVEELE----
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; Pred. No. 0.48;
22; Mismatches 47; Indels
                                                                                                                                                                            Score 108; DB Pred. No. 0.44;
                                                                                                                                                          Mismatches
                                                                                                                                                                                                      DB 2;
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Tondella, M.L.C.; Matsumoto
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                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-143 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A; Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flagellar protein required for flagellar formation fliL [imported] - Bacillus halodur
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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A; Residues: 1-461 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMEC-----RNVTHLLQQEL 74
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LVNIMLIILIVLTLVGVAVLIFVNYFNNEDEQDREPTIDEIIAQSYETEEITTNLLSNDF 65
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26.1%; Pred. No. 0.52;
ative 28; Mismatches
                                                                                                         12.0%; Score 107; DB 22.1%; Pred. No. 0.17;
                                                                                      Mismatches
                                                                                                                                  DB 2;
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A;Cross-references: GB:M55532; NID:g203362; PIDN:AAA40892.1; PID:g203363 R;Hoyle, G.W.; Hill, R.L. J. Biol. Chem. 263, 7487-7492, 1988 A;Title: Molecular cloning and sequencing of a cDNA for a carbohydrate b. A;Reference number: A28166; MUID:88227939 A;Accession: A28166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kupffer cell receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 05-Nov-1999
C;Accession: A38674; A28166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribosome receptor, 180k - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Oct-1999
C;Accession: A56734
R;Wanker, E.E.; Sun, Y.; Savitz, A.J.; Meyer, D.I.
J. Cell Biol. 130, 29-39, 1995
                                                                                                                            A;Cross-references: GB:J03734; NID:g205050;
;Superfamily: C-type lectin homology
C;Keywords: transmembrane protein
C;Keywords: transmembrane protein
F;412-536/Domain: C-type lectin homology <LC
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A; Residues: 1-550 <HO2>
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J. Biol. Chem. 266, 1850-1857, 1991
Title: Structure of the gene for a carbohydrate-binding receptor unique Reference number: A38674, MUID:91107689
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Residues: 1-1534 <WAN>
Residues: 1-1534 <WAN>
Residues: 1-1534 <WAN>
R;Cross-references: GB:X87224; NID:g984113; PIDN:CAA60676.1; PID:g984114
C;Keywords: endoplasmic reticulum; membrane protein; protein biosynthesis
F;198-743/Region: 10-residue repeats (N-Q-G-K-K-A-E-G-A-P)
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A; Accession: A56734
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A; Residues: 1-550 < HOY>
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"~+~hes 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEA------QKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAAVAKSKLREVNKELAAEKAKAAAGEAKVKKQLVAREQEITAVQARIEASYREHVKEVQ 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQD---DINALMQEGSVVKI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEGEITTLNHKLQDA-SAEVERLRRENQVL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                               lectin homology <LCH>
                                        11.5%;
28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%;
28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 102.5;
Pred. No. 4.4;
                                        Score 102;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                  Mismatches
                                                                                                                                                                                                 PIDN: AAA41472.1; PID: g205051
                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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                                                          Length 550;
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                  14;
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-415 <PODD>
A;Cross references: EMBL:X69324; NID:g311759;
R;Haanes, E.J.; Heath, D.G.; Cleary, P.P.

PIDN:CAA49165.1;

PID:g311760

submitted to the EMBL Data A; Reference number: S35760 A; Accession: S35760

Library,

November 1992

forA protein precursor - Streptococcus (Species: Streptococcus pyogenes C;Date: 13-Jan-1995 #sequence\_revision C;Accession: S35760; A42711 R;Podbielski, A.

pyogenes 13-Jan-1995

#text\_change

26-Aug-1999

RESULT S35760

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C;Accession: JX0209; PX0009
R;Sato, M.; Kawakami, K.; Osawa, T.;
J. Biochem. 111, 331-336, 1992
                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: glycoprotein; lectin; macrophage; transmembrane protein F;36-61/Domain: transmembrane #status predicted <TRA> F;173-296/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 102-120;137, 'X', 139-151 <ODA>
C; Superfamily: hepatic lectin; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Oda, S.; Sato, M.; Toyoshima, S.; Osawa, J. Biochem. 104, 600-605, 1988
A;Title: Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning and expression of A;Reference number: JX0209; MUID:92268032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: PX0009; MUID:89197865
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A; Residues: 1-304 <SAT>
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Best Local
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144
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                                                                             84
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                                                                                                                                                             41 LGLSLLLLVVVSVIG-------SQNSQLRRDLGTLRATLD--NTTSKIKAE------F
                                                                                                                                                                                                    24 LGIGILVLLIIVILGVPLIIFTIKANSEACRD--GLRAVMECRNVTHLLQQELTEAQKGF
                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactose/N-acetylgalactosamine-specific -
DHVQQLRKDLKALTCQLANLK----NNGSEVACCP 174
                                    AEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEVQSLKTGLEA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAQ-LKSTSSLNSQIEVVNGKLKDSSRELQTLRRD---LSDVSALKSNVQMLQSNLQKAK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISAEIQAMRDGMQRAGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLDAE 105
                                                                             QSLDSRADSFEKGISSLKVDVEDHRQELQAGRDLSQKVTSLESTVEKREQALKTDLSDLT
                                                                                                                    QDVEAQAATCNHTVMALMASLDAEKAQGQ~~~~~KKVEELEGEI~~~~TTLNHKLQDAS
                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                 11.2%;
23.2%;
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                                                                                                                                                                                                                                                               Score 99.5;
Pred. No. 1.
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                                                                                                                                                                                                                                           Gaps
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                                                                                                                    131
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A; Molecule type: DNA
A; Residues: 847-1333,'R',1335-1876,'L',1878-1963
R; Willis, N.; Gesteland, R.F.; Karn, J.; Barnett,
Cell 33, 575-583, 1983
A; Title: The genes sup-7 X and sup-5 III of Caeno
A; Reference number: A21074
A; ACCESSION: A21074
A; MOLECULE type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 174, 4967-4976, 1992
A;Title: Architecture of the vir regulons of group A streptococci parallels opacity A;Title: Architecture of the vir regulons of group A streptococci parallels opacity A;Reference number: A42711; MUID:92332431
A;Accession: A42711
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 343-415 <HAA>
A;Residues: 343-415 <HAA>
A;Cross-references: GB:M86806; NID:g153630; PIDN:AAA26887.1; PID:g153631
A;Experimental source: Strain CS101, OF+
A;Mote: sequence extracted from NCBI backbone (NCBIN:108942, NCBIP:108945)
C;Superfamily: M5 protein
                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
A; Residues: 1-1963 <WIZ>
A; Cross-references: EMBL: Z83107; PIDN: CAB05505.1; GSPDB: GN
A; Cross-references: EMBL: Z83107; PIDN: CAB05505.1; GSPDB: GN
A; Experimental source: clone F32A7
R; Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A; Title: Protein structural domains in the Caenorhabditis
A; Reference number: A93958; MUID: 83273600
A; Accession: A93958
                                                                                                                                                                                                                                                              A;Cross-references: GB:J01050; R;McLachlan, A.D.; Karn, J. Nature 299, 226-231, 1982
                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, A; Reference number: Z19322
A; Accession: T20770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myosin heavy chain B [similarity] - Caenorhabditis elegans N;Contains: myosin ATPase (EC 3.6.1.32) C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 13-Jun-1983 #sequence_revision 19-May-2000 #text_change 19-Jan-2001 C;Accession: T20770; T21629; A93958; A93287; A21074; A02992 R;Kershaw, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Дb
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A; Residues: 1-1963 <WIL>
A; Cross-references: EMBL: Z81499; PIDN: CAB04089.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
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Pred. No. 2.
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                                                                       Caenorhabditis elegans
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                                                                                                                     Bolten, S.; Waterston,
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                                                                                                                                                                                                                                                                                                                                                                                                                          unc-54 myosin
                                                                       suppress
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                                                                                                                       R.H.
                                                                            amber
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RESULT

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F:662-684/Region: actin binding #status predicted F:766-780/Region: actin binding #status predicted F:768-780/Region: actin binding #status predicted <CO F:848-1963/Domain: coiled coil #status predicted <CO F:848-1162/Region: S2 F:1163-1963/Region: light meromyosin F:1163-1963/Region: light meromyosin F:125/Modified site: N6,N6-trimethyllysine (Lys) F:180/Binding site: ATP (Lys) #status predicted F:702,712/Active site: Cys #status predicted
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F;74-181/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Barroso, M.; Nelson, D.S.; Sztul, E.
Proc. Natl. Acad. Sci. U.S.A. 92, 527-531, 1995
A;Title: Transcytosis-associated protein (TAP)/pl15
A;Reference number: A55913; MUID:95132633
A;Accession: A55913
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                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-959 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcytosis-associated protein pl15 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999
C;Accession: A55913
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853
                                          178 LLQ 180
                                                                                       793
                                                                                                                                                                                739 IEELRSHQVLLQSQLAEKDTVIENLRSSQVSGMSEQALATCSPRDAE-----
                                                                                                                                                                                                                        60 VMECRNVTHLLQQELTEAQKGFQDV-EAQAATCNHTVMALMASLDAEKAQGQKKVEELEG 118
                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                       ELSALKSQLCSQSLEITRLQTENRELQQRAETLAKSVPVEGESELVTAAKTTDVEGRLSA
                                                                                                                               EITTLNHKLQDASAEVERLRRENQVLSVRIAD-KKYYPSSQDSSSAAAPQLLIVLLGLSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNFERLQDLIDKLQQKLKTQKKQVEEAE-ELANLNLQKYKQLTHQLEDAEERAD--QAEN
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37; Conserv
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30.1%;
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24.78;
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Pred. No. 12;
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A:Map position: 1
A:Map position: 1
A:Introns: 23/3; 114/3; 229/1; 264/1; 320/1; 857/3; 1745/3; 1814/1; 1892/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino ac
E:87-773/Domain: myosin motor domain homology <MMOT>
E:177-184/Region: nucleotide-binding motif A (P-loop)
3:660-682/Region: actin binding #status predicted
E:846-1938/Domain: coiled coil #status predicted
E:846-1938/Domain: coiled coil #status predicted
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A;Recession: A02993
A;Molecule type: DNA
A;Residues: 24-93,'E',95-97,'R',99-376,'V',378-388,'GDV',392-407,'N',409-473,'G',475-57
A;Residues: 24-93,'E',95-97,'R',99-376,'V',378-388,'GDV',392-407,'N',409-473,'G',475-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: clone R06C7 R;Dibb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J. J. Mol. Biol. 205, 603-613, 1989 A;Title: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain A;Reference number: S02771; MUID:89178677 A;Accession: S02772
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C;Accession: T21193; T23973; S02772; A02993
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A; Accession: T23973
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A;Residues: 1-1938 <WIL>
A;Cross-references: EMBL.Z71261; PIDN:CAA95806.1; GSPDB:GN00019; CESP:R06C7.10
A;Experimental source: clone F21C3
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R; McMurray, A.
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N;Contains: myosin ATPase (EC 3.6.1.32)
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N;Alternate names:
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Best Local
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   AAPQLLIV 171
                                                          GEGLYGSEELEELKRKQMNRVMDLQEALSAA----
                                                                                                              AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSA 163
                                                                                                                                                                            KAAEDELHERQEFHAACKNLEHELDQCHELLEEQINGKDDIQRQLSRINSEISQWKARYE 1383
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26.6%;
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Pred.
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No.
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13;
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puff II/9A-2 protein precursor - fungus gnat (Sciara coprophila)
C;Species: Sciara coprophila
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
C;Accession: S07533
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Ωy
                                                                                                                                C;Keywords: coiled coil; glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-286/Product: puff II/9A protein #status predicted <W
F;156/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                         J. Mol. Biol. 210, 531-540, 1989
A;Title: Molecular characterization of DNA
A;Reference number: S07532; MUID:90133907
A;Accession: S07533
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C; Date: 09-Jun-2000
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A; Residues: 1-286 <DIB>
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R; Hawkins, T.; Thomas, K.
submitted to the EMBL Data Library, October 1993
A; Reference number: $40997
A; Cocession: $40998
Status: preliminary
A; Molecule type: DNA
A; Residues: 1-597 (HAW)
A; Cross-references: EMBL: 227081
C; Genetics:
A; Introns: 40/3; 76/1; 125/1; 199/1; 240/1; 274/1; 292/3; 392/3; 429/2; 486/2; 521/1
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C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
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earch completed: July 18, 2002, 18:43:58 time: 181 sec
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US-08-98-342-4
US-09-113-788-4
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US-08-247-636-2
US-08-247-491A-3
US-08-319-795-2
US-08-468-985-2
US-08-469-985-2
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US-08-809-494A-2
US-09-352-302-2
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5210183-3	5210183-2	US-09-071-709-1	US-09-071-709-9	US-08-995-654-3	US-08-700-178-3	US-08-402-217A-3	US-08-247-491A-5	US-08-468-718-4	US-08-467-852A-5	US-08-214-222-4	US-08-469-434-4	US-08-072-070-4	US-08-482-847-23	US-08-127-499A-23	US-08-446-201-3	US-08-247-491A-2	US-08-468-718-2
Patent No. 5210183	Patent No. 5210183	Sequence 1, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	23,	Sequence 23, Appl	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli

#### ALIGNMENTS

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Sequence 1, Application US/08624650 Patent No. 5914252
                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/JP94/01732

FILING DATE: 14-OCT-1994

PRIOR APPLICATION DATA: PFILING DATE: JP 5-281622

APPLICATION NUMBER: JP 5-281622

FILLING DATE: 15-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24.618

REGISTRATION NUMBER: 24.618
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,650
FILING DATE: 22-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                  TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                               REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HIRANO, TOSHIO
APPLICANT: KAISHO, TSUNEYASU
TITLE OF INVENTION: MEMBRANE
TITLE OF INVENTION: PRE-B CEL
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: V
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                                       STRANDEDNESS:
                                                                                   LENGTH:
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                                                               amino acid
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1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                 180 amino acids
                        linear
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                                         single
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Query Match Best Local :

Local Similarity

100.0%; Score 889; DB 2; 100.0%; Pred. No. 4.3e-88;

Conservative

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Mismatches

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Length 180;

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                                                                  Matches
                                                                                    Query Match
Best Local
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INFORMATION FOR SEQ ID NO: 4:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: GenBa
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Y. Tom
APPLICANT: Patterson, Chandra
APPLICANT: Corley, Neil C.
APPLICANT: Sather, Susan
TITLE OF INVENTION: HUMAN OXII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TTLNHKLQDASAEVERLRRENQVLSVRIADKKYYPSSQDSSSAAAPQLLIVLLGLSALLQ 180
40 VLCLGLLVTVILLILQLSQVSDLIKKQQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/0 FILING DATE: Filed Herewith CLASSIFICATION:
                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: li
                               23 LLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQ 82
                                                                                                                                                                     CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                  Similarity
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3174 Porter Dr.
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IBM Compatible
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                                                                 11.2%; Score 99.5; DB 2
25.9%; Pred. No. 0.0068;
tive 25; Mismatches 4
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----ANITH--QEDILEGQ----
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                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                           Matches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sawamura, Tatsuya APPLICANT: Masaki, Tomoo
 143 VLSVRIADKKYY--PSSQD 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                         Local Similarity nes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24
REFERENCE/DOCKET NUMBER:
                                           81
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CITY: New York
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                                                                                                                                                    23 LLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                            DVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQ 142
                                                                                                                 VLCLGLLVTVILLILQLSQVSDLIKKQQ-----ANITH--QEDILEGQ---- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQ 142
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5. 5962260
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                                         --ILAQRRSEKS-AQESQKELKEMIETLAHKLDEKSKKLMELHRQNL 124
                                                                                                                                                                                                           11.2%; Score 99.5; DB 2; 25.9%; Pred. No. 0.0068;
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NLQEVLKEAANYSGPCPQD 143

APPLICANT: Masaki, Tomoo

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                               Sequence 4, Application US/08809494A Patent No. 5962260
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 7-2
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLDDETS, JULES E
REGISTRATION NUMBER: 24408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: JG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sawamura, Tat:
APPLICANT: Masaki, Tomoo
                                                                                                                                   125
                                                                                                                                                                  143 VLSVRIADKKYY -- PSSQD 159
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
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                                                                                                                                                                                                                                                               40 VLCLGLLYTVILLILQLSQVSDLIKKQQ------ANITH--QEDILEGQ----
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                                                                                                                                                                                                                                 83 DVEAQAATCNHTYMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQ 142
                                                                                                                                                                                                                                                                                                  23 LLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEAQKGFQ 82
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Sawamura, Tatsuya
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PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                   Length 270;
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Query Match
Best Local Similarity
Matches 36; Conserva
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                                                                                                                                                 Sequence 4, Application US/09352302 Patent No. 6197937
                                                                                                                                   GENERAL INFORMATION:
                                                     APPLICANT: Sawamura, Tatsu
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modifi
TITLE OF INVENTION: Recept
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212 818-9479 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 6-321705 FILING DATE: 30-NOV-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                          CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                           128 NLQEVLKEAANYSGPCPQD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 273 amino acids TYPE: amino acid
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ADDRESSEE: MCAULU,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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25.9%;
                                                          Modified Low-Density Lipoprotein Receptor 8
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Pred. No. 0.
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COUNTRY:

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10016-2391

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; MOLECULE TYPE:
US-09-352-302-4
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LENGTH: 273 amino acid
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REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
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APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
APPLICATION NUMBER: JP 7-214206
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                         APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael
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   COMPUTER:
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                                                                         COUNTRY:
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E: Floppy disk
IBM PC compatible
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                                                                                                                            Harness, Dickey & Pierce, P.L.C
O. Box 828
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                                                                                                                                                                                               Rearrangements
                                                                                                                                                                                                                Markers for Detection of Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 99.5; DB 4; 25.9%; Pred. No. 0.0069;
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; MOLECULE TYPE:
US-08-533-306A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Best Local
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                TELEFAX: (810) 641-02: INFORMATION FOR SEQ ID NO:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Smith, DeAnn F.
                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE:
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hes 27; Conserv
                                                                                                                                                     APPLICATION NUMBER: FILING DATE: NO. 58 CLASSIFICATION: 435
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                                                                                                    NAME: Smith, DeAnn F. REGISTRATION NUMBER: 36683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 CRDGLRAVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNHTVMALMASLD------ 103
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GY: linear
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P.O. Box 828
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                                (810) 641-0270
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                                                   (810) 641-1600
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                                                                                                                                                                        R: US/08/742,923A
5869611ember 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rearrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Markers for Detection of Chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                        Dickey & Pierce, P.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michael J.
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4ER: 2115-00869COB
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                                                                                       2115-00869DVC
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Qy
                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-938-105-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                 1753 ALKGGKKQLQKLEARVRELENEL-----EAEQKRNAESVKGMRKSERRIKELTYQTEEDK 1807
                                                                                                        1693 AVQECRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNMEQTIKDLQHRLDEAEQI 1752
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Leinwand, APPLICANT: Vikstrom,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                     108 Q----GOKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKY----YPSSQDS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 -AEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 CSDGERARAELNDKVHKLQNEVESVTGMLNEAEGKAIKLAKDVASLSSQLQDTQELLQEE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 TRQKLNVSTKLRQLEEERNSLQDQLDEEMEAKQNLERHISTLNIQLSDSK 324
161 SSAAAPQLLIVLLGL 175
                                                                                                                                                                                                                                                                                                                                         LENGTH: 1886 amino acids
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                                                                                                                                      59 AVMECRNVTHLLQQELTEAQKGFQDVEAQAATCNH------TVMALMASLD-AEKA 107
                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Denver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                              10.5%; Score 93.5; DB 24.4%; Pred. No. 0.46;
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Karen L.
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                              Sequence 4, Application US/09113788 Patent No. 5969104 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
APPLICANT:
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FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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LIBRARY: GenBa
CLONE: 1235724
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LENGTH: 292 amino acid
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   APPLICANT:
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MOLECULE TYPE:
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TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
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                                                                                                                                                                                                                                                                    144
                                                                                                                                                                                                                                                                                                      124 NHKLQDASAE 133
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                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 CHILLSLGLGLLLLVIICVVGF-----QNSKFQRDLVTLRTDFSNFTSNTVAEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 CKLL--LGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEA | || || || :| :| :| || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: 
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                                                                                                                                                                                                                                                                NNNGEEASTE
                                                                                                                                                                                                                                                                                                                                                                                              ----QALTSQGSSLEETIASLKAEVEGFKQERQAVHSEMLLRVQQLVQDLKKLTCQVATL 143
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Au-Young, Janice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.48; 24.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92.5; Db 2;
Pred. No. 0.043;
"'Amatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0095-1 CIP
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Cocks, Benjamin G.

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US-09-111-470-4
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                                                                                                                                                 Patent No.
                                                                                                                                                   Sequence 4, Application US/09111470 Patent No. 6277959
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                GENERAL INFORMATION:
APPLICANT: Vallad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: per IMMEDIATE SOURCE: LIBRARY: GenBanl CLONE: 1235724
                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                  APPLICANT:
                                                                                APPLICANT:
                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
                                                                                                                                                                                                                                                       144 NNNGEEASTE 153
                                                                                                                                                                                                                                                                                     124 NHKLQDASAE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 POR CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                      88 ----QALTSQGSSLEETIASLKAEVEGFKQERQAVHSEMLLRVQQLVQDLKKLTCQVATL 143
                                                                                                                                                                                                                                                                                                                                                                                                                   20 CKLL--LGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELTEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/113,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                     39 CHLLLSLGLGLLLLVIICVVGF-----QNSKFQRDLVTLRTDFSNFTSNTVAEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                     QKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ------KKVEELEGEITTL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank
                               Lebecque,
                                                 Saeland, Sem
                                                                                Bates, Elizabeth E.M
                                                                                                  Ravel, Odile
                                                                Ford, John
                                                                                                                Valladeau, Jenny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.4%; Score 92.5; DB 24.6%; Pred. No. 0.043;
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Mammalian Membrane Protein Genes; Related Reagents
                                 Serge J.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 292;
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                                                                                     ; SOFTWARE: FastSEQ for Windows Version 4.0
; SEO ID NO 1
; LENGTH: 1939
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-310-187A-1
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-310-187A-1
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APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09310187A Patent No. 6358751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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APPLICATION NUMBER: US 60/053,080

FILING DATE: 09-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: SF0695

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650,0852-9196
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/310,187A CURRENT FILING DATE: 1999-05-12 NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                         TITLE OF INVENTION: Involvement of Autoantigens TITLE OF INVENTION: Graft Rejection FILE REFERENCE: UCSF-090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650)496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 0
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 ----QALTSQGSSLEETIASLKAEVEGFKQERQAGVSELQEHTTQKAH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 QKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNH 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 CHLLLSLGLGLLLLVIICVVGF-----QNSKFQRDLVTLRTDFSNFTSNTVAEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 316 amino acids amino acid
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 Conservative
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27.8%; Pred. No. 0.1;
                 10.1%;
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 28;
                   Score 89.5;
Pred. No. 1
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 316;
                                    DB 4;
 51;
                                                                                                                                                                                                                                                                                               in Cardiac
                                  Length 1939;
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 Indels
   23;
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RESULT 15
US-08-446-201-4
; Sequence 4, Application US/08446201B
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                                                                                                                                                                                                                                                       Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 840-07 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/312,949
FILING DATE: 30-SEP-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER: WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Briles, David
APPLICANT: Wu, Hong-Yin
TITLE OF INVENTION: MUCC
TITLE OF INVENTION: PNEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1861 KNLLRLQDLVDKLQL 1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1746 AVQECRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNMEQTIKDLQHRLDEAEQI 1805
                                                                                                225
                                                                                                                                  111 K-----KVEELEGEITTLNHKLQDA--SAEVERLRENQVLSVRIADKK 152
                                                                                                                                                                      178 TAELENQVHRLEQELKEIDESESEDYAKEGFR------APLQSKLDAKKAKLS 224
                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
                                                                                                                                                                                                             60 VMECRNVTHLLQQELTE------AQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSAAAPQLLIVLLGL 175
                                                                                                KLEELSDKIDELDAEIAKLEDQLKAAEENNNVEDYFKEG--LEKTIAAKK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q----GQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIADKKY----YPSSQDS 160
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                                                                                                                                                                                                                                                                                                                                                                                                                      : 288 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curtis, Morris & Safford, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                       9.9%; Score 88; DB 3; Length 288; 30.9%; Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUCOSAL ADMINISTRATION OF
                                                                                                                                                                                                                                                   15; Mismatches
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CURRENT FILING DATE: 1995-05-19
EARLIER APPLICATION NUMBER: 08/312,949
EARLIER FILING DATE: 1994-09-30
EARLIER APPLICATION NUMBER: 08/246,636
EARLIER FILING DATE: 1994-05-20
EARLIER APPLICATION NUMBER: 08/048,896
EARLIER FILING DATE: 1993-04-20
EARLIER FILING DATE: 1993-04-20
EARLIER APPLICATION NUMBER: 07/835,698
EARLIER APPLICATION NUMBER: 07/835,698
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SEQ ID NO 4
LENGTH: 288
                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR MUCOSAL ADMINISTRATION OF TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN A (PSPA) FILE REFERENCE: 454312-2018
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 07/
EARLIER FILING DATE: 1991-02-15
NUMBER OF SEQ ID NOS: 4
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                        111 K-----KVEELEGEITTLNHKLQDA--SAEVERLRRENQVLSVRIADKK 152
                                                                                              178 IAELENQVHRLEQELKEIDESESEDYAKEGFR-----,-APLQSKLDAKKAKLS 224
                                                                                                                                             60 VMECRNVTHLLQQELTE-----AQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQ 110
KLEELSDKIDELDAEIAKLEDQLKAAEENNNVEDYFKEG--LEKTIAAKK 272
                                                                                                                                                                                            34;
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                  9.9%; Score 88; DB 3 30.9%; Pred. No. 0.13;
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                                                                                                                                                                                                                                        DB 3;
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Search completed: July 18, 2002, 18:42:58 Job time: 276 sec

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